

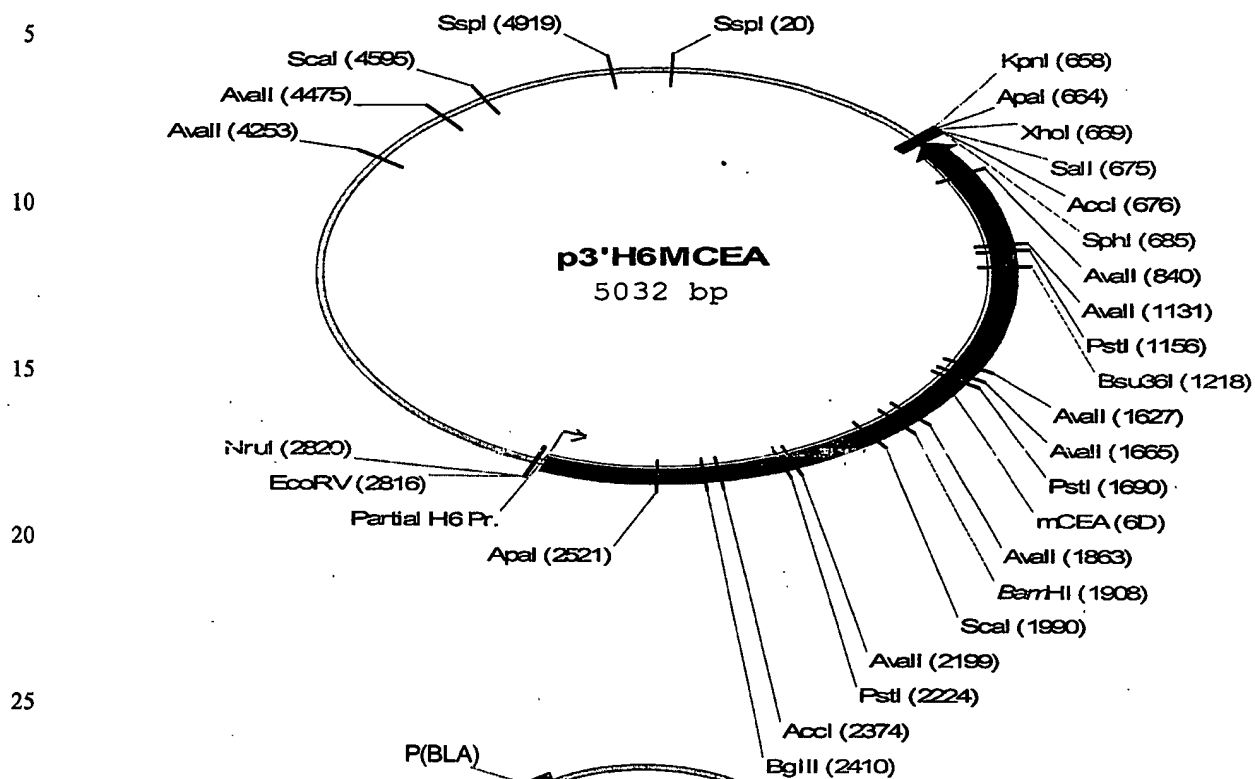
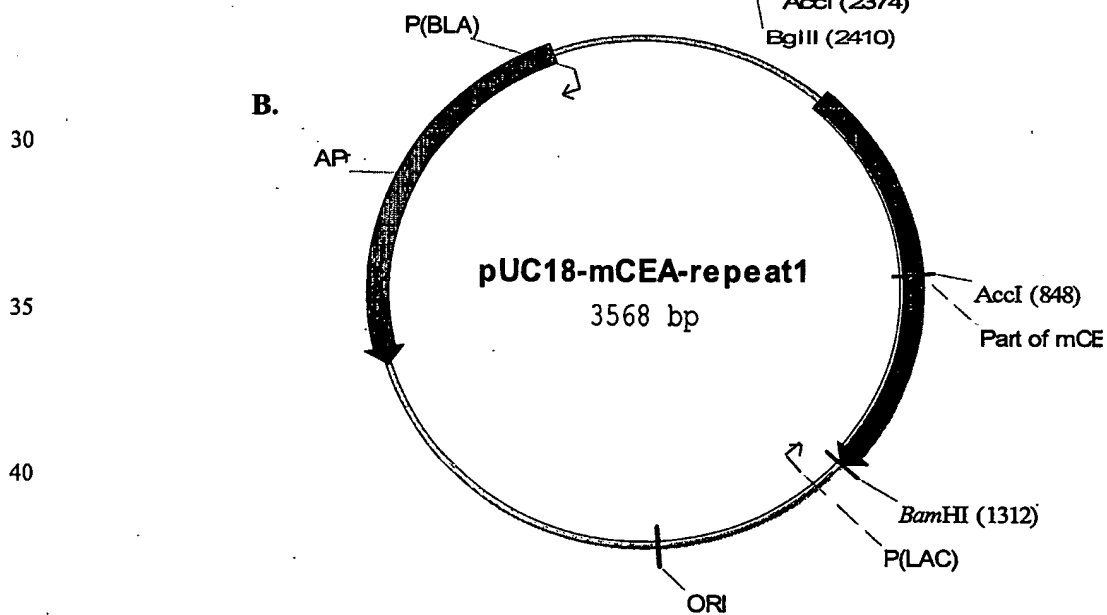
FIGURE 1**A.****B.**

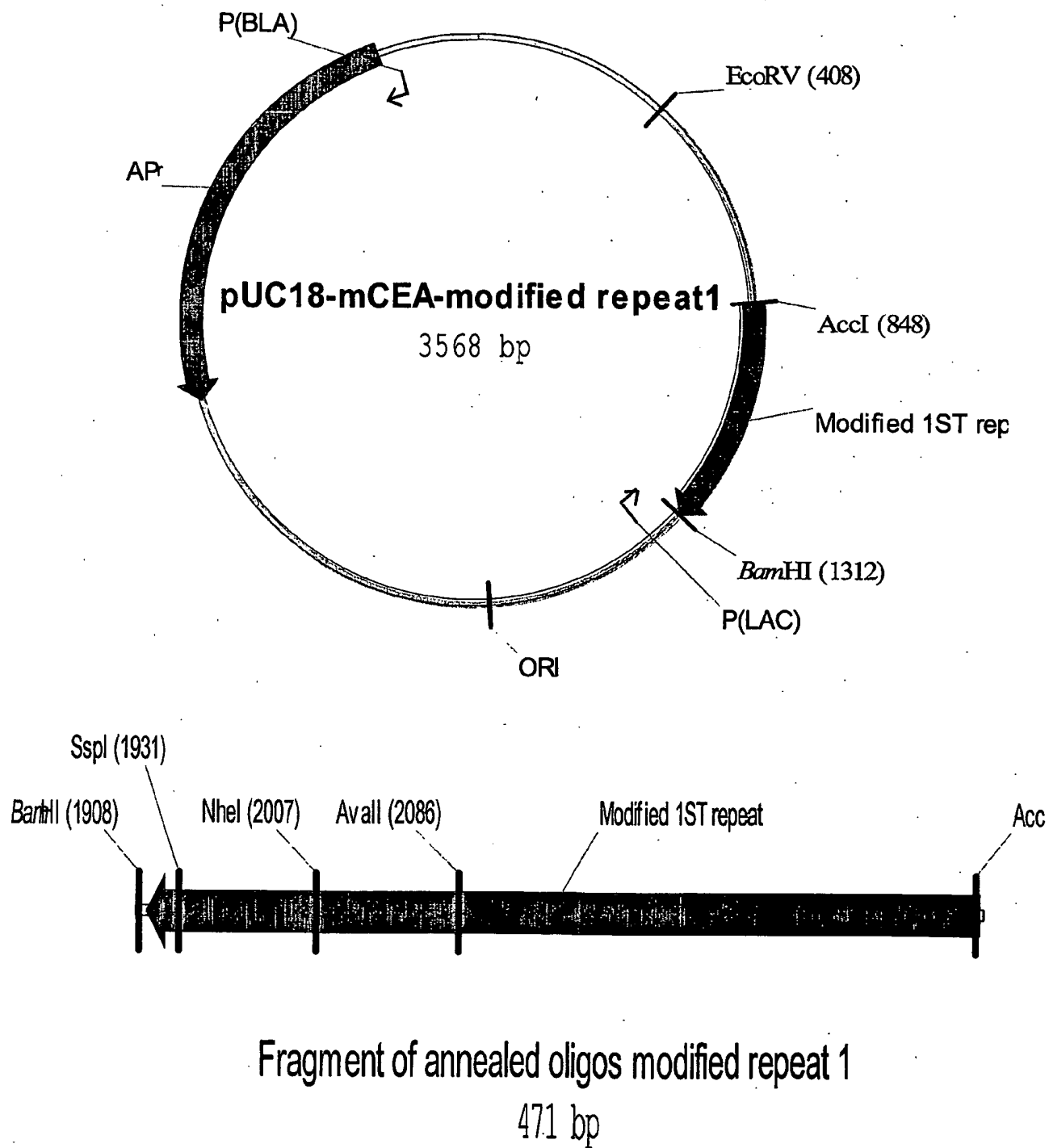
FIGURE 2

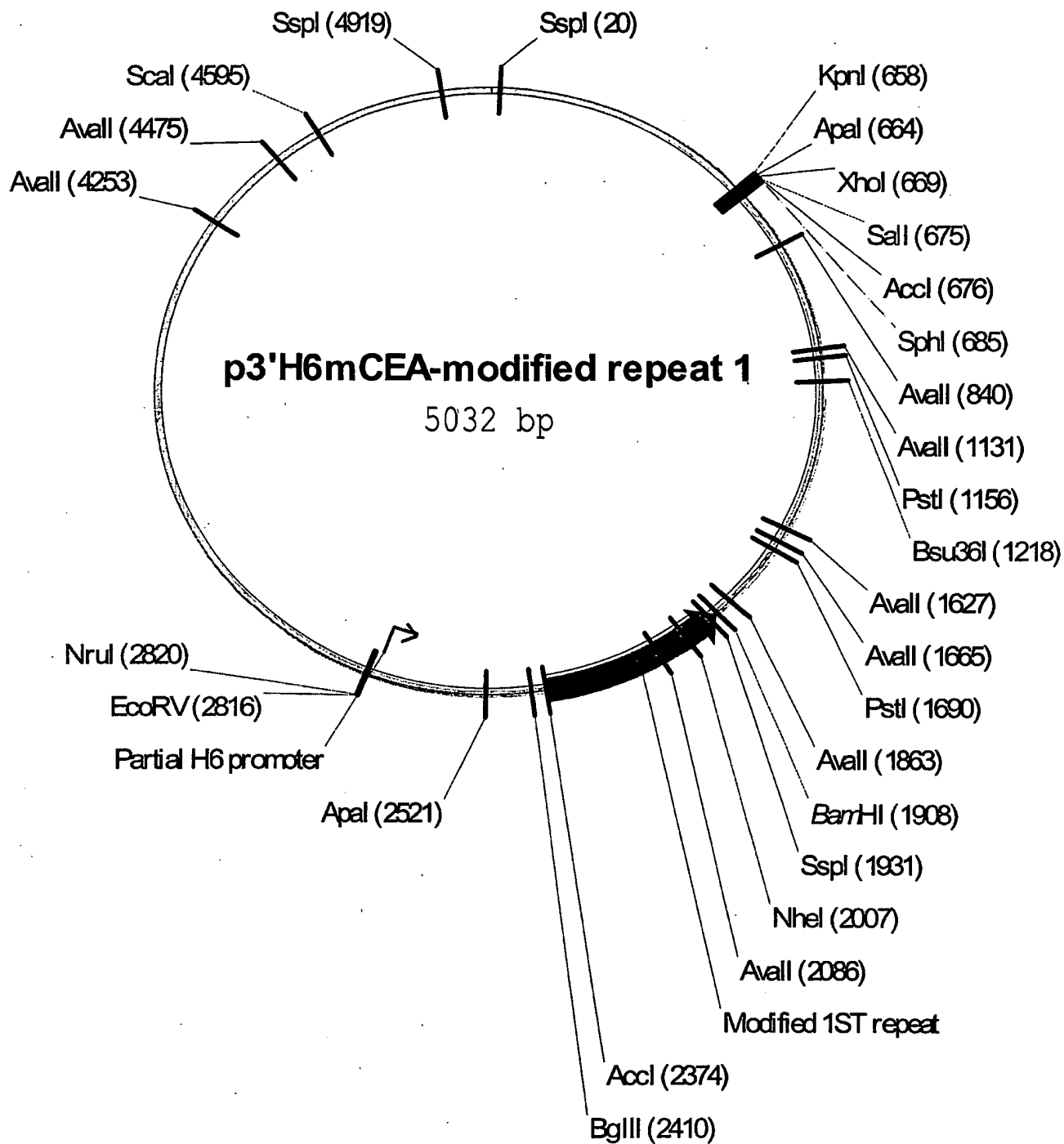
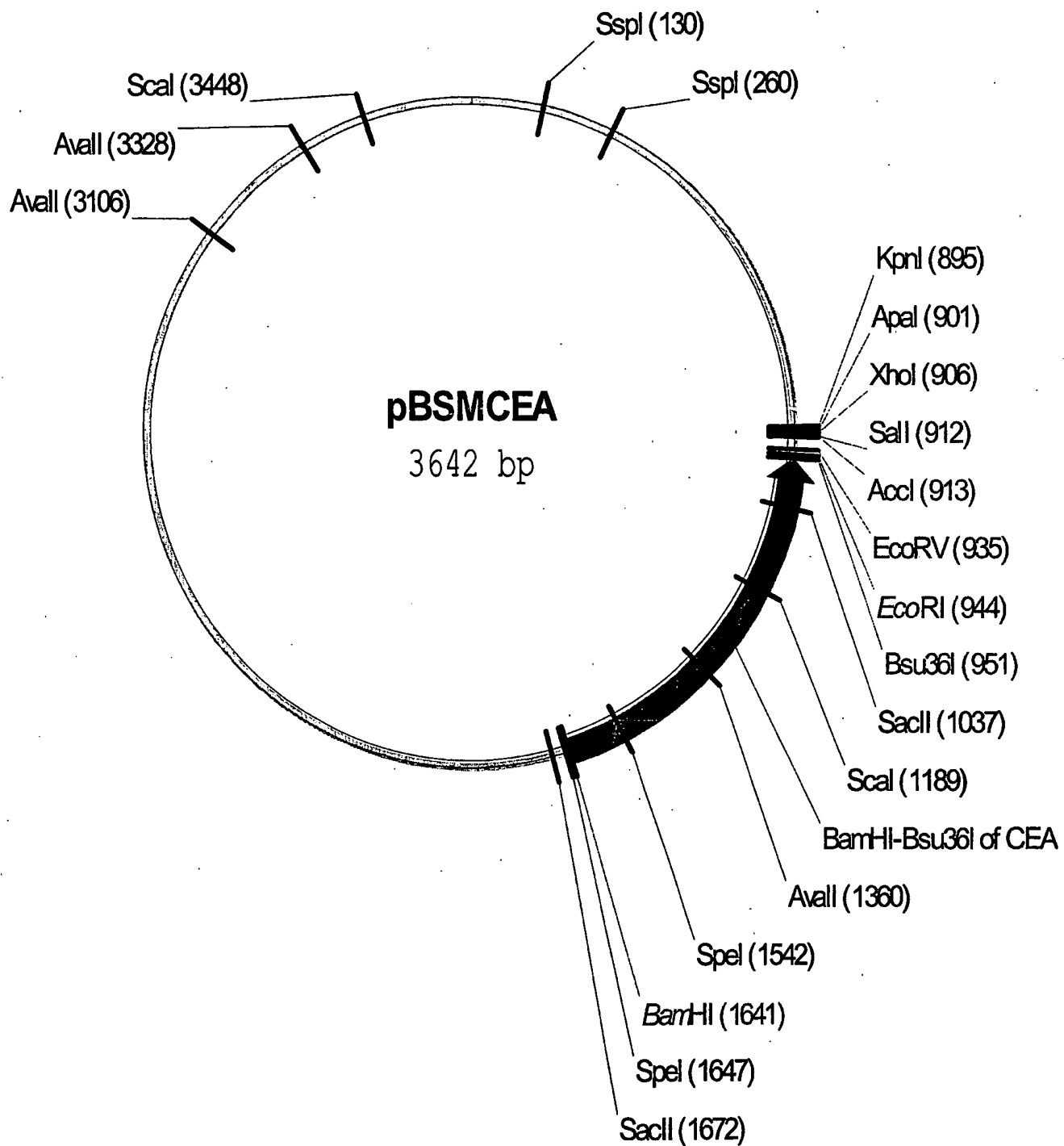
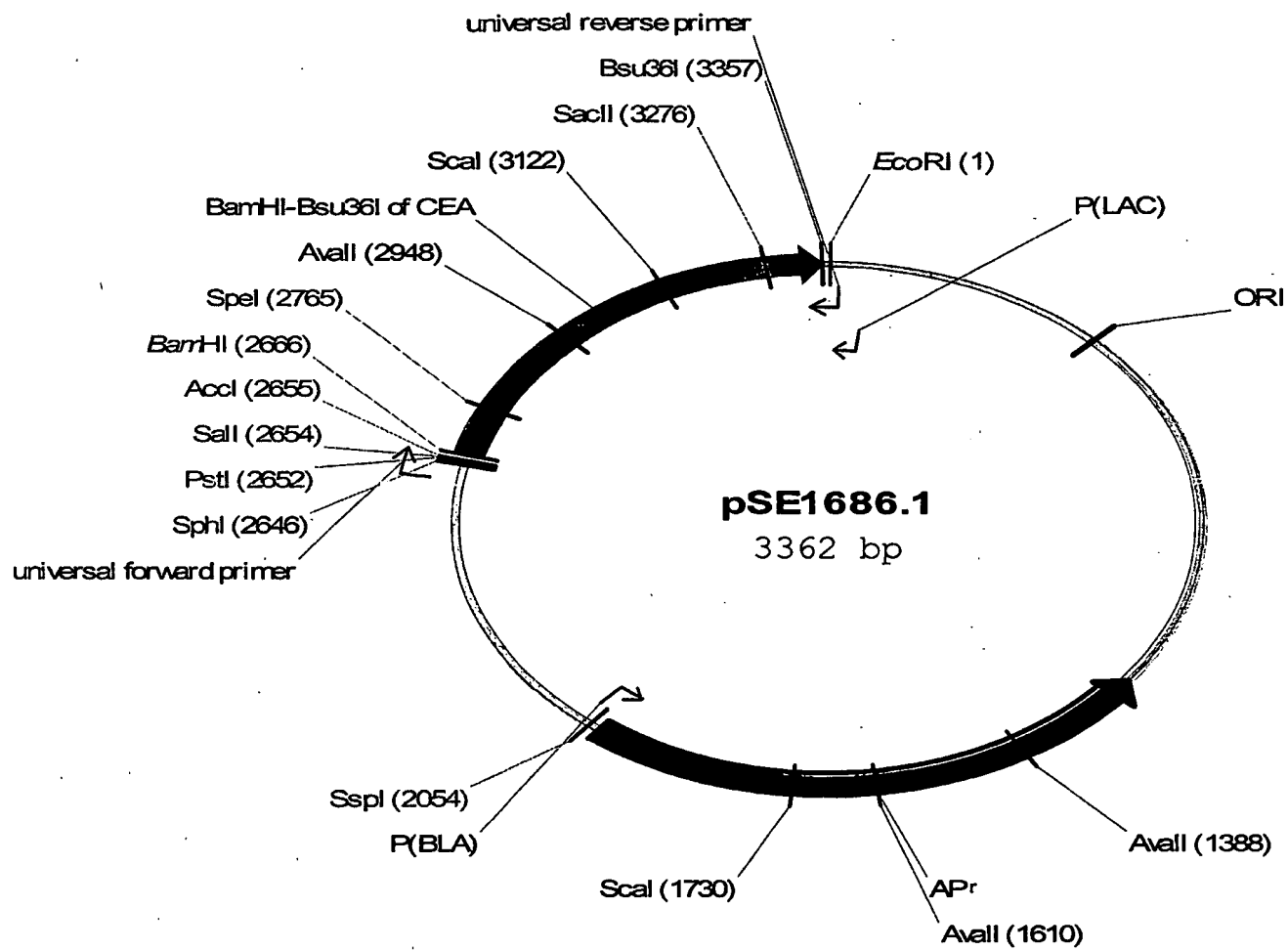
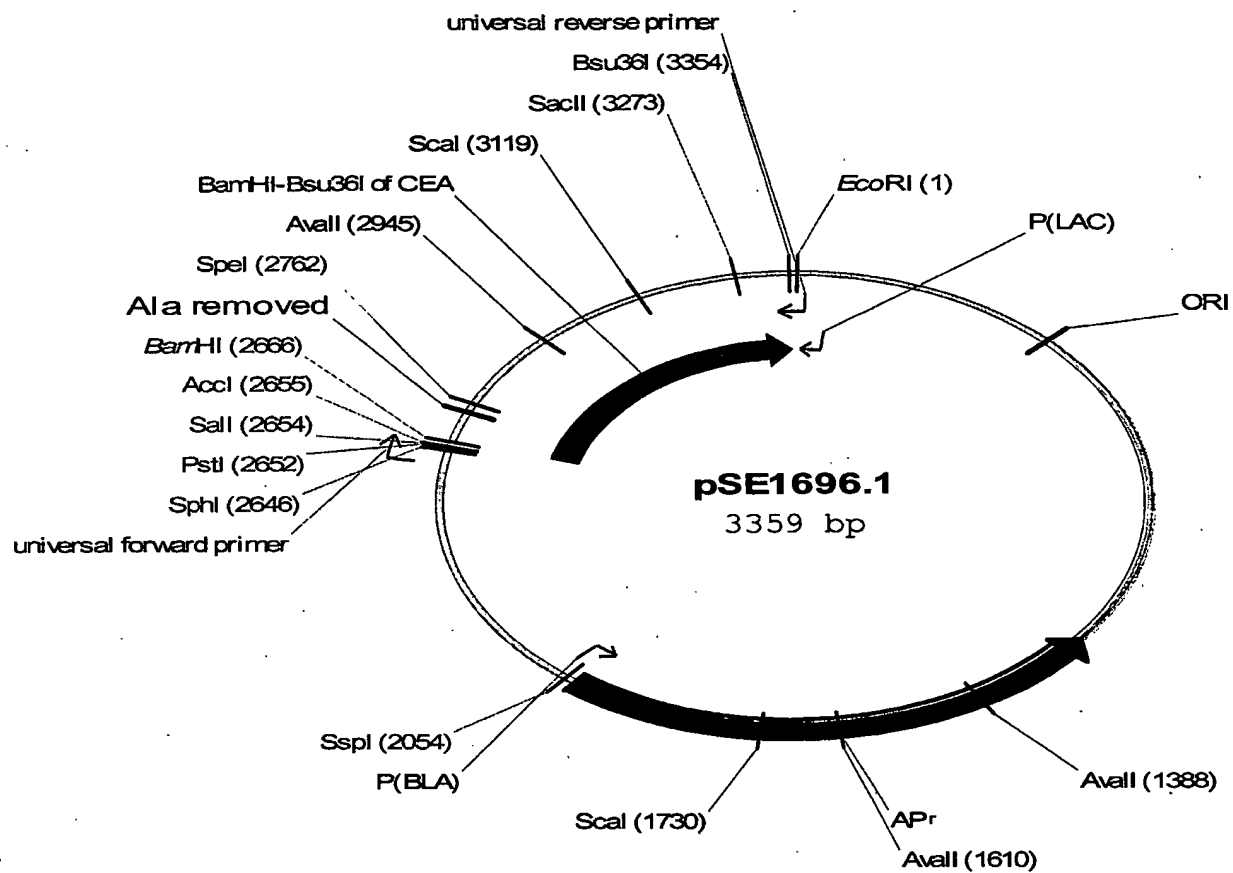
FIGURE 3

FIGURE 4

5/29

FIGURE 5**pUC18 mCEA modified repeat 2 (gsoe)**

6/29

FIGURE 6

pUC18 mCEA modified repeat 2 gsoe minus Ala

FIGURE 7

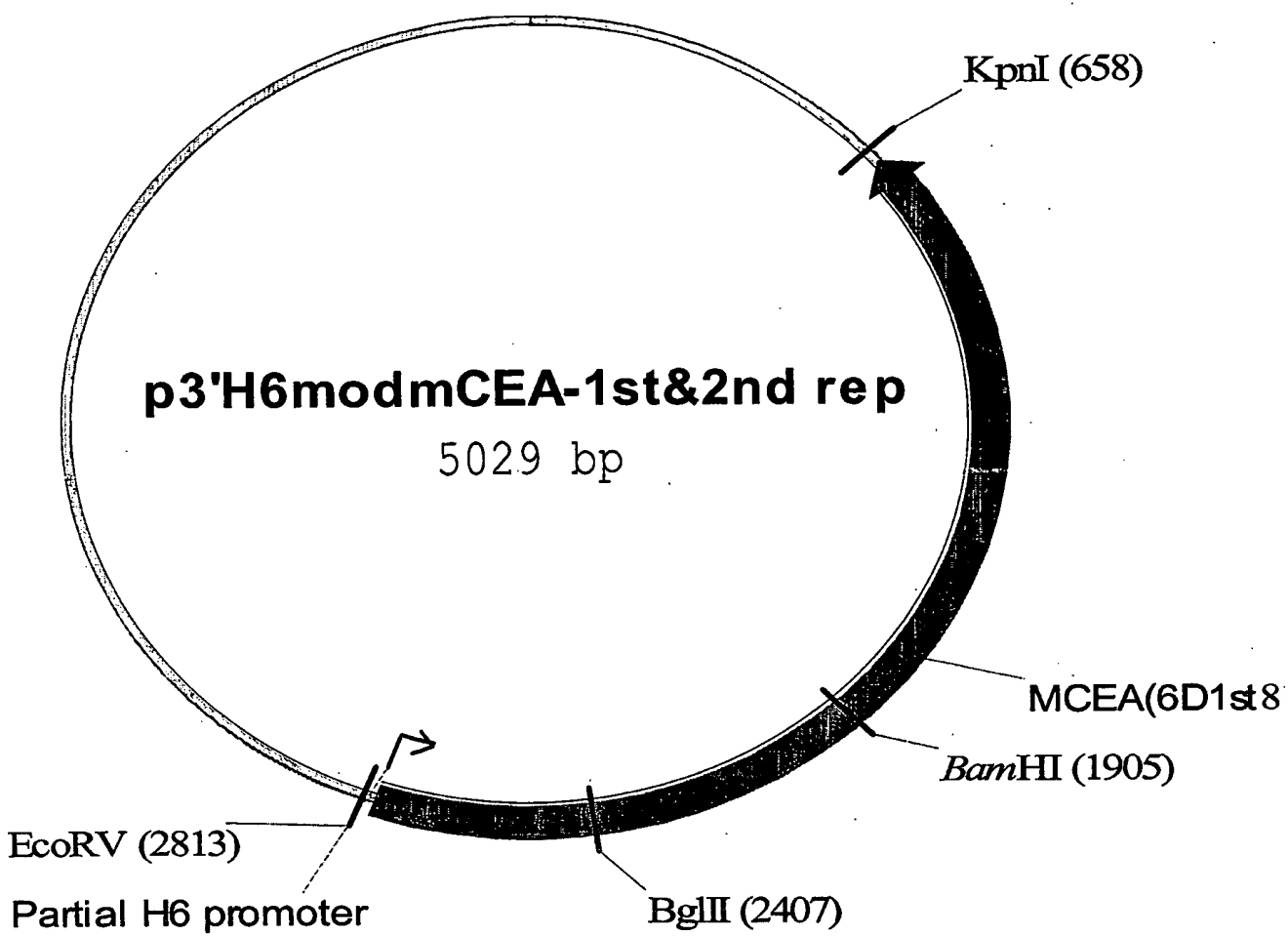
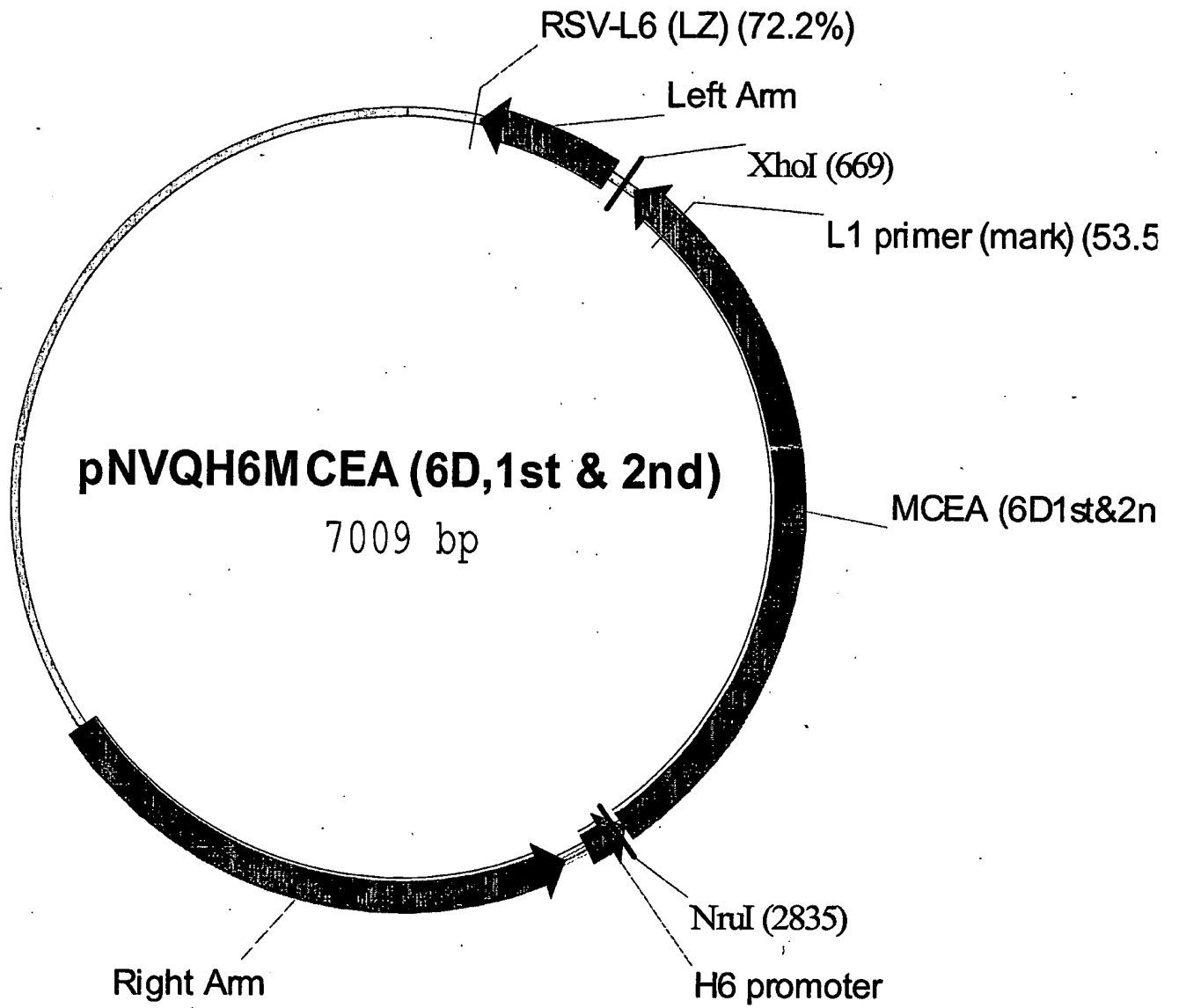


FIGURE 8



9/29

FIGURE 9A

		1		50
	mCEA (6D)	ATGGAGTCTC CCTCGGCCCC TCCCCACAGA TGGTGCATCC CCTGGCAGAG		
5	mCEA (6D, 1st&2nd)	ATGGAGTCTC CCTCGGCCCC TCCCCACAGA TGGTGCATCC CCTGGCAGAG		
		51		100
	mCEA (6D)	GTCCTGCTC ACAGCCTCAC TTCTAACCTT CTGGAACCCG CCCACCACTG		
10	mCEA (6D, 1st&2nd)	GTCCTGCTC ACAGCCTCAC TTCTAACCTT CTGGAACCCG CCCACCACTG		
		101		150
	mCEA (6D)	CCAAGCTCAC TATTGAATCC ACGCCGTTCA ATGTCGCAGA GGGGAAGGAG		
	mCEA (6D, 1st&2nd)	CCAAGCTCAC TATTGAATCC ACGCCGTTCA ATGTCGCAGA GGGGAAGGAG		
15		151		200
	mCEA (6D)	GTGCTTCTAC TTGTCCACAA TCTGCCCCAG CATCTTTTGG GCTACAGCTG		
	mCEA (6D, 1st&2nd)	GTGCTTCTAC TTGTCCACAA TCTGCCCCAG CATCTTTTGG GCTACAGCTG		
		201		250
20	mCEA (6D)	GTACAAAGGT GAAAGAGTGG ATGGCAACCG TCAAATTATA GGATATGTAA		
	mCEA (6D, 1st&2nd)	GTACAAAGGT GAAAGAGTGG ATGGCAACCG TCAAATTATA GGATATGTAA		
		251		300
25	mCEA (6D)	TAGGAACTCA ACAAGCTACC CCAGGGCCCC CATACTAGTG TCGAGAGATA		
	mCEA (6D, 1st&2nd)	TAGGAACTCA ACAAGCTACC CCAGGGCCCC CATACTAGTG TCGAGAGATA		
		301		350
	mCEA (6D)	ATATACCCCA ATGCATCCCT GCTGATCCAG AACATCATCC AGAATGACAC		
30	mCEA (6D, 1st&2nd)	ATATACCCCA ATGCATCCCT GCTGATCCAG AACATCATCC AGAATGACAC		
		351		400
	mCEA (6D)	AGGATTCTAC ACCCTACACG TCATAAAGTC AGATCTTGTG AATGAAGAAG		
	mCEA (6D, 1st&2nd)	AGGATTCTAC ACCCTACACG TCATAAAGTC AGATCTTGTG AATGAAGAAG		
35		401		450
	mCEA (6D)	CAACTGGCCA GTTCCGGGTA TACCCGGAGC TGCCCAAGCC CTCCATCTCC		
	mCEA (6D, 1st&2nd)	CAACTGGCCA GTTCCGGGTA TACCCGGAAC TCCCTAAGCC TTCTATTAGC		
		451		500
40	mCEA (6D)	AGCAACAACCT CCAAACCCGT GGAGGACAAG GATGCTGTGG CCTTCACCTG		
	mCEA (6D, 1st&2nd)	<u>TCCAATAATA</u> <u>GTAAGCCTGT</u> <u>CGAAGACAAA</u> <u>GATGCCGTGC</u> <u>CTTTTACATG</u>		
		501		550
45	mCEA (6D)	TGAACCTGAG ACTCAGGACG CAACCTACCT GTGGTGGGTA AACAATCAGA		
	mCEA (6D, 1st&2nd)	<u>CGAGCCCGAA</u> <u>ACTCAAGACG</u> <u>CAACATATCT</u> <u>CTGGTGGGTG</u> <u>AACAACCAGT</u>		
		551		600
	mCEA (6D)	GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CAGGACCCTC		
50	mCEA (6D, 1st&2nd)	<u>CCCTGCCTGT</u> <u>GTCCCCTAGA</u> <u>CTCCAACCTCA</u> <u>GCAACGGAAA</u> <u>TAGAACCTCTG</u>		
		601		650
	mCEA (6D)	ACTCTATTCA ATGTCACAAG AAATGACACA GCAAGCTACA AATGTGAAAC		
	mCEA (6D, 1st&2nd)	<u>ACCCTGTTTA</u> <u>ACGTGACCAG</u> <u>GAACGACACA</u> <u>GCAAGCTACA</u> <u>AATGCGAAAC</u>		

10/29

FIGURE 9B

		651		700		
	mCEA (6D)	CCAGA <u>A</u> CCCA	GTGAGTGCCA	GGCGCAGTGA	TTCAGTCATC	CTGAATGTCC
5	mCEA (6D, 1st&2nd)	CCAAAAT <u>T</u> CCA	GT <u>C</u> AGC <u>G</u> CCA	GGAGGT <u>T</u> CTGA	TTCAGT <u>G</u> ATT	CT <u>CA</u> ACGTGC
		701		750		
	mCEA (6D)	TCTATGGCCC	GGATGCCCC	ACCATT <u>T</u> TCCC	CTCTAAACAC	ATCTTACAGA
	mCEA (6D, 1st&2nd)	TTTACGG <u>A</u> CC	CGATGCT <u>C</u> CT	ACAAT <u>C</u> AGCC	CTCTAAACAC	AAGCTAT <u>AGA</u>
10		751		800		
	mCEA (6D)	TCAGGGGAAA	ATCTGAACCT	CTCCTGCCAC	GCAGCCTCTA	ACCCACCTGC
	mCEA (6D, 1st&2nd)	TCAGGGGAAA	ATCTGAATCT	<u>G</u> AGCTGT <u>C</u> AT	GCCGCTAG <u>CA</u>	ATCCT <u>CCC</u> GC
15		801		850		
	mCEA (6D)	ACAGTACTCT	TGGTTTGTC	ATGGGACTTT	CCAGCAATCC	ACCCAAGAGC
	mCEA (6D, 1st&2nd)	<u>C</u> CAATAC <u>A</u> GC	TGGTTTGTC	ATGGC <u>A</u> CTTT	CCA <u>A</u> CAGTCC	ACCCAGGA <u>A</u> C
20		851		900		
	mCEA (6D)	TCTTTATCCC	CAACATCACT	GTGAATAATA	GTGGATCCTA	TACGTGCCAA
	mCEA (6D, 1st&2nd)	TGTTCA <u>T</u> TCC	CAATATT <u>A</u> CC	GTGAACAATA	GTGGATCCTA	<u>C</u> ACGTGCCAA
25		901		950		
	mCEA (6D)	GCCCATAACT	CAGACACTGG	CCTCAATAGG	ACCACAGTCA	CGACGATCAC
	mCEA (6D, 1st&2nd)	GCTCACA <u>ATA</u>	<u>G</u> CGACAC <u>CG</u> G	<u>A</u> CTCAAC <u>CG</u> C	ACA <u>A</u> CCGT <u>GA</u>	CGACGATT <u>A</u> C
30		951		1000		
	mCEA (6D)	AGTCTATGAG	CCACCCAAAC	CCTTCATCAC	CAGCAACAAC	TCCAACCCCG
	mCEA (6D, 1st&2nd)	<u>C</u> GTGTATGAG	CCACCA <u>AA</u> AC	<u>C</u> ATT <u>C</u> ATAAC	<u>T</u> AGTAACAAT	TCTA <u>ACC</u> CAG
35		1001		1050		
	mCEA (6D)	TGGAGGATGA	GGATGCTGTA	GCCTTAACCT	GTGAACCTGA	GATTGAGAAC
	mCEA (6D, 1st&2nd)	TTGAGGATGA	GGACGCAGTT	GCATTAACTT	GTGAGCCAGA	GATT <u>CAAA</u> T
40		1051		1100		
	mCEA (6D)	ACAACCTACC	TGTGGTGGGT	AAATAATCAG	AGCCTCCCGG	TCAGTCCCAG
	mCEA (6D, 1st&2nd)	ACC <u>A</u> CTTAT <u>T</u>	TATGGTGGGT	<u>CA</u> ATAAC <u>CA</u> A	AGTTTGC <u>CG</u> G	TTAG <u>CCC</u> ACG
45		1101		1150		
	mCEA (6D)	GCTGCAGCTG	TCCAATGACA	ACAGGACCCT	CACTCTACTC	AGTGTACAA
	mCEA (6D, 1st&2nd)	<u>C</u> TTGCAGTTG	TCTAATGATA	ACCGC <u>A</u> CATT	<u>G</u> ACACTCCTG	<u>T</u> CCGTTACTC
50		1151		1200		
	mCEA (6D)	GGAATGATGT	AGGACCCTAT	GAGTGTGGAA	TCCAGAACGA	ATTAAGTGTT
	mCEA (6D, 1st&2nd)	GCAATGATGT	AGGACCTTAT	GAGTGTGGCA	T <u>T</u> CAGAATGA	ATTAT <u>CC</u> GTT
55		1201		1250		
	mCEA (6D)	GACCACAGCG	ACCCAGTCAT	CCTGAATGTC	CTCTATGGCC	CAGACGACCC
	mCEA (6D, 1st&2nd)	GAT <u>C</u> ACT <u>CC</u> G	ACCCTGTTAT	CCTTAATGTT	<u>T</u> TGTATGGCC	CAGACGACCC
60		1251		1300		
	mCEA (6D)	CACCATTTCC	CCCTCATACA	CCTATTACCG	TCCAGGGGTG	AACCTCAGCC
	mCEA (6D, 1st&2nd)	AACATATCT	CCATCATACA	CCTACTACCG	TCCCGGCGTG	AACCTGAGCC

11/29

FIGURE 9C

		1301		1350		
	mCEA (6D)	TCTCCTGCCA	TGCAGCCTCT	AACCCACCTG	CACAGTATTC	TTGGCTGATT
5	mCEA (6D, 1st&2nd)	<u>TTTCT</u> TGCCA	TGCAGC <u>ATCC</u>	<u>AACCCC</u> CCTG	CACAGT <u>ACTC</u>	<u>CTGGCT</u> GATT
		1351		1400		
	mCEA (6D)	GATGGGAACA	TCCAGCAACA	CACACAAGAG	CTCTTTATCT	CCAACATCAC
	mCEA (6D, 1st&2nd)	GATGG <u>AA</u> ACA	<u>TT</u> CAGCAG <u>CA</u>	<u>TACT</u> CAAGAG	<u>TTATTT</u> TATA <u>AA</u>	<u>GCAACATA</u> AA
10		1401		1450		
	mCEA (6D)	TGAGAAGAAC	AGCGGACTCT	ATACCTGCCA	GGCCAATAAC	TCAGCCAGTG
	mCEA (6D, 1st&2nd)	TGAGAAGAAC	AGCGGACTCT	ATACT <u>T</u> GCCA	GGCCAATAAC	TCAGCCAGTG
15		1451		1500		
	mCEA (6D)	GCCACAGCAG	GACTACAGTC	AAGACAATCA	CAGTCTCTGC	GGAGCTGCCC
	mCEA (6D, 1st&2nd)	<u>GTC</u> ACAGCAG	GACTACAG <u>TT</u>	<u>AAA</u> ACAATA <u>AA</u>	<u>CTGT</u> <u>TT</u> CCGC	GGAGCTGCCC
20		1501		1550		
	mCEA (6D)	AAGCCCTCCA	TCTCCAGCAA	CAACTCCAAA	CCCGTGGAGG	ACAAGGATGC
	mCEA (6D, 1st&2nd)	AAGCCCTCCA	TCTCCAGCAA	CAACTCCAAA	CCCGTGGAGG	ACAAGGATGC
25		1551		1600		
	mCEA (6D)	TGTGGCCTTC	ACCTGTGAAC	CTGAGGCTCA	GAACACAACC	TACCTGTGGT
	mCEA (6D, 1st&2nd)	TGTGGCCTTC	ACCTGTGAAC	CTGAGGCTCA	GAACACAACC	TACCTGTGGT
30		1601		1650		
	mCEA (6D)	GGGTAAATGG	TCAGAGCCTC	CCAGTCAGTC	CCAGGCTGCA	GCTGTCCAAT
	mCEA (6D, 1st&2nd)	GGGTAAATGG	TCAGAGCCTC	CCAGTCAGTC	CCAGGCTGCA	GCTGTCCAAT
35		1651		1700		
	mCEA (6D)	GGCAACAGGA	CCCTCACTCT	ATTCAATGTC	ACAAGAAATG	ACGCAAGAGC
	mCEA (6D, 1st&2nd)	GGCAACAGGA	CCCTCACTCT	ATTCAATGTC	ACAAGAAATG	ACGCAAGAGC
40		1701		1750		
	mCEA (6D)	CTATGTATGT	GGAATCCAGA	ACTCAGTGAG	TGCAAACCGC	AGTGACCCAG
	mCEA (6D, 1st&2nd)	CTATGTATGT	GGAATCCAGA	ACTCAGTGAG	TGCAAACCGC	AGTGACCCAG
45		1751		1800		
	mCEA (6D)	TCACCCTGGA	TGTCCTCTAT	GGGCCGGACA	CCCCATCAT	TTCCCCCCCCA
	mCEA (6D, 1st&2nd)	TCACCCTGGA	TGTCCTCTAT	GGGCCGGACA	CCCCATCAT	TTCCCCCCCCA
50		1801		1850		
	mCEA (6D)	GACTCGTCTT	ACCTTTTCGGG	AGCGGACCTC	AACCTCTCCT	GCCACTCGGC
	mCEA (6D, 1st&2nd)	GACTCGTCTT	ACCTTTTCGGG	AGCGGACCTC	AACCTCTCCT	GCCACTCGGC
		1851		1900		
	mCEA (6D)	CTCTAACCCA	TCCCCGCAGT	ATTCTTGGCG	TATCAATGGG	ATACCGCAGC
	mCEA (6D, 1st&2nd)	CTCTAACCCA	TCCCCGCAGT	ATTCTTGGCG	TATCAATGGG	ATACCGCAGC
		1901		1950		
	mCEA (6D)	AACACACACA	AGTTCTCTTT	ATCGCCAAAA	TCACGCCAAA	TAATAACGGG
	mCEA (6D, 1st&2nd)	AACACACACA	AGTTCTCTTT	ATCGCCAAAA	TCACGCCAAA	TAATAACGGG

12/29

FIGURE 9D

		1951		2000		
	mCEA (6D)	ACCTATGCCT	GTTTTGTCTC	TAACTTGGCT	ACTGGCCGCA	ATAATTCCAT
5	mCEA (6D, 1st&2nd)	ACCTATGCCT	GTTTTGTCTC	TAACTTGGCT	ACTGGCCGCA	ATAATTCCAT
		2001		2050		
	mCEA (6D)	AGTCAAGAGC	ATCACAGTCT	CTGCATCTGG	AACTTCTCCT	GGTCTCTCAG
10	mCEA (6D, 1st&2nd)	AGTCAAGAGC	ATCACAGTCT	CTGCATCTGG	AACTTCTCCT	GGTCTCTCAG
		2051		2100		
	mCEA (6D)	CTGGGGCCAC	TGTCGGCATC	ATGATTGGAG	TGCTGGTTGG	GGTTGCTCTG
	mCEA (6D, 1st&2nd)	CTGGGGCCAC	TGTCGGCATC	ATGATTGGAG	TGCTGGTTGG	GGTTGCTCTG
15		2101				
	mCEA (6D)	ATATAG				
	mCEA (6D, 1st&2nd)	ATATAG				

FIGURE 10

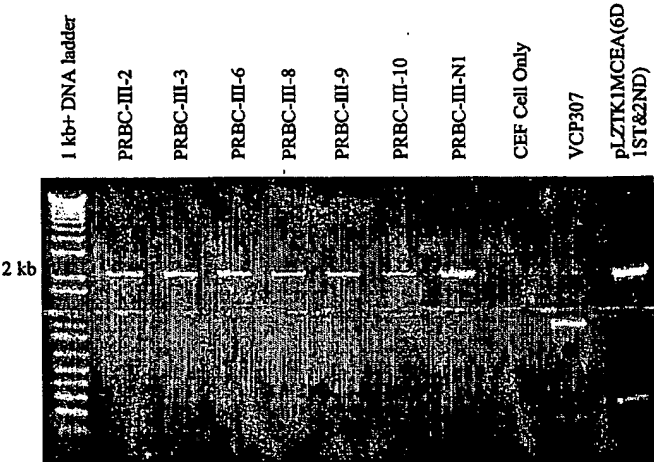
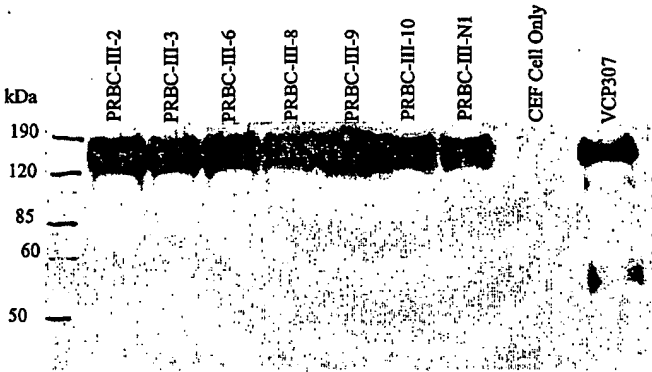
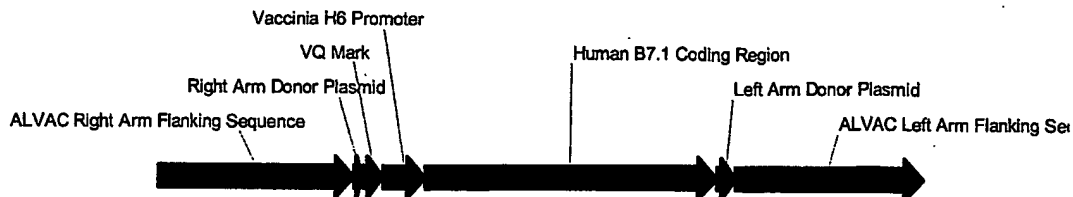


FIGURE 11

5



10

FIGURE 12

ALVAC Right Arm Flanking Sequence
 ~~~~~  
 1 TTAGATTGTG TTATTCATTA CATAGACGCT GCTAAATCTA CTATCGATTT  
 AATCTAACAC AATAAGTAAT GTATCTGCGA CGATTAGAT GATAGCTAAA

ALVAC Right Arm Flanking Sequence  
 ~~~~~  
 51 AGAGATAGTA TCTCTACTAC CCACAAAAG AACTAAAGAC GCCATAGTGT
 TCTCTATCAT AGAGATGATG GGTGTTTTTC TTGATTCTG CGGTATCACA

ALVAC Right Arm Flanking Sequence
 ~~~~~  
 101 ACTGGCCTAT AATAAAAGAC GCGTTGATAA GAGCTGTTCT GGAACGTGGT  
 TGACCGGATA TTATTTTCTG CGCAACTATT CTCGACAAGA CCTGCACCA

ALVAC Right Arm Flanking Sequence  
 ~~~~~  
 151 GTTAACTTA GAATACTACT AGGTTATTGG AAAAGACCG ATATTATCTC
 CAATTTGAAT CTTATGATGA TCCAATAACC TTTTCTGGC TATAATAGAG

ALVAC Right Arm Flanking Sequence
 ~~~~~  
 201 TAAAGCTTCT ATCAAAGTC TTAATGAGTT AGGTGTAGAT AGTATAGATA  
 ATTTGGAAGA TAGTTTTCAG AATTACTCAA TCCACATCTA TCATATCTAT

ALVAC Right Arm Flanking Sequence  
 ~~~~~  
 251 TTACTACAAA GGTATTCATA TTTCTATCA ATTCTAAAGT AGATGATATT
 AATGATGTTT CCATAAGTAT AAAGGATAGT TAAGATTTC TCTACTATAA

ALVAC Right Arm Flanking Sequence
 ~~~~~  
 301 AATAACTCAA AGATGATGAT AGTAGATAAT AGATACGCTC ATATAATGAC  
 TTATTGAGTT TCTACTACTA TCATCTATTA TCTATGCGAG TATATTACTG

ALVAC Right Arm Flanking Sequence  
 ~~~~~  
 351 TGCAAATTTG GACGGTTCAC ATTTTAATCA TCACGCGTTC ATAAGTTTCA
 ACGTTTAAAC CTGCCAAGTG TAAATTAGT AGTGCGCAAG TATTCAAAGT

ALVAC Right Arm Flanking Sequence

401 ACTGCATAGA TCAAAATCTC ACTAAAAAGA TAGCCGATGT ATTTGAGAGA
TGACGTATCT AGTTTTAGAG TGATTTTCT ATCGGCTACA TAAACTCTCT

ALVAC Right Arm Flanking Sequence

451 GATTGGACAT CTAACACGC TAAAGAAATT ACAGTTATAA ATAATACATA
CTAACCTGTA GATTGATGCG ATTTCTTTAA TGTCAATATT TATTATGTAT

ALVAC Right Arm Flanking Sequence

501 ATGGATTTTG TTATCATCAG TTATATTTAA CATAAGTACA ATAAAAAGTA
TACCTAAAC AATAGTAGTC AATATAAATT GTATTCATGT TATTTTTCAT

Right Arm Donor Plasmid

ALVAC Right Arm Flanking Sequence

551 TTAAATAAAA ATACTACTT ACGAAAAAT GACTAATTAG CTATAAAAC
AATTTATTTT TATGAATGAA TGCTTTTCTA CTGATTAATC GATATTTTG

VQ Mark

Right Arm Donor Plasmid

601 CCGGGTTAAT TAATTAGTTA TTAGACAAGG TGAAAACGAA ACTATTTGTA
GGCCAATTA ATTAATCAAT AATCTGTTCC ACTTTTGCTT TGATAACAT

VQ Mark

Vaccinia H6 Promoter

651 GCTTAATTAA TTAGAGCTTC TTTATTCTAT ACTTAAAAAG TGAAAATAAA
CGAATTAATT AATCTCGAAG AAATAAGATA TGAATTTTTC ACTTTTATTT

Vaccinia H6 Promoter

701 TACAAAGGTT CTTGAGGTT GTGTTAAATT GAAAGCGAGA AATAATCATA
ATGTTTCCAA GAACTCCCAA CACAATTTAA CTTTCGCTCT TTATTAGTAT

Human B7.1 Coding Region

Vaccinia H6 Promoter

751 AATTATTTCA TTATCGCGAT ATCCGTTAAG TTTGTATCGT AATGGGCCAC
TTAATAAAGT AATAGCGCTA TAGGCAATTC AACATAGCA TTACCCGGTG

Human B7.1 Coding Region

801 ACACGGAGGC AGGGAACATC ACCATCCAAG TGTCCATACC TCAATTTCTT
TGTGCCTCCG TCCCTTGTAG TGGTAGGTTT ACAGGTATGG AGTTAAAGAA

Human B7.1 Coding Region

851 TCAGCTCTTG GTGCTGGCTG GTCTTTCTCA CTTCTGTTCA GGTGTTATCC
AGTCGAGAAC CACGACCGAC CAGAAAGAGT GAAGACAAGT CCACAATAGG

Human B7.1 Coding Region

~~~~~  
901 ACGTGACCAA GGAAGTGAAA GAAGTGGCAA CGCTGTCCTG TGGTCACAAT  
TGCACCTGGTT CCTTCACTTT CTTCACCGTT GCGACAGGAC ACCAGTGTTA

## Human B7.1 Coding Region

~~~~~  
951 GTTCTGTGTT AAGAGCTGGC ACAAACTCGC ATCTACTGGC AAAAGGAGAA
CAAAGACAAC TTCTCGACCG TGTTTGAGCG TAGATGACCG TTTTCCTCTT

Human B7.1 Coding Region

~~~~~  
1001 GAAAATGGTG CTGACTATGA TGTCTGGAGA CATGAATATA TGGCCCAGT  
CTTTTACCAC GACTGATACT ACAGACCTCT GTACTTATAT ACCGGGCTCA

## Human B7.1 Coding Region

~~~~~  
1051 ACAAGAACCG GACCATCTTT GATATCACTA ATAACCTCTC CATTGTGATC
TGTTCTTGGC CTGGTAGAAA CTATAGTGAT TATTGGAGAG GTAACACTAG

Human B7.1 Coding Region

~~~~~  
1101 CTGGCTCTGC GCCCATCTGA CGAGGGCACA TACGAGTGTG TTGTTCTGAA  
GACCGAGACG CGGGTAGACT GCTCCCGTGT ATGCTCACAC AACAGACTT

## Human B7.1 Coding Region

~~~~~  
1151 GTATGAAAAA GACGCTTTCA AGCGGGAACA CCTGGCTGAA GTGACGTTAT
CATACTTTTT CTGCGAAAGT TCGCCCTTGT GGACCGACTT CACTGCAATA

Human B7.1 Coding Region

~~~~~  
1201 CAGTCAAAGC TGACTTCCCT ACACCTAGTA TATCTGACTT TGAAATTCCA  
GTCAGTTTCG ACTGAAGGGA TGTGGATCAT ATAGACTGAA ACTTTAAGGT

## Human B7.1 Coding Region

~~~~~  
1251 ACTTCTAATA TTAGAAGGAT AATTGCTCA ACCTCTGGAG GTTTTCCAGA
TGAAGATTAT AATCTTCCTA TTAAACGAGT TGGAGACCTC CAAAAGGTCT

Human B7.1 Coding Region

~~~~~  
1301 GCCTCACCTC TCCTGGTTGG AAAATGGAGA AGAATTAAAT GCCATCAACA  
CGGAGTGGAG AGGACCAACC TTTTACCTCT TCTTAATTTA CGGTAGTTGT

## Human B7.1 Coding Region

~~~~~  
1351 CAACAGTTTC CCAAGATCCT GAAACTGAGC TCTATGCTGT TAGCAGCAAA
GTTGTCAAAG GGTTCAGGA CTTTGACTCG AGATACGACA ATCGTCGTTT

Human B7.1 Coding Region

~~~~~  
1401 CTGGATTTC AATATGACAAC CAACCACAGC TTCATGTGTC TCATCAAGTA  
GACCTAAAGT TATACTGTTG GTTGGTGTCG AAGTACACAG AGTAGTTCAT

## Human B7.1 Coding Region

~~~~~  
1451 TGGACATTTA AGAGTGAATC AGACCTTCAA CTGGAATACA ACCAAGCAAG
ACCTGTAAAT TCTCACTTAG TCTGGAAGTT GACCTTATGT TGGTTCGTTC

Human B7.1 Coding Region

~~~~~  
1501 AGCATTTTCC TGATAACCTG CTCCCATCCT GGGCCATTAC CTTAATCTCA  
TCGTAAAAGG ACTATTGGAC GAGGGTAGGA CCCGGTAATG GAATTAGAGT

## Human B7.1 Coding Region

~~~~~  
1551 GTAAATGGAA TTTTCGTGAT ATGCTGCCTG ACCTACTGCT TTGCCCCAGC
CATTACCTT AAAAGCACTA TACGACGGAC TGGATGACGA AACGGGGTGC

Human B7.1 Coding Region

~~~~~  
1601 CTGCAGAGAG AGAAGGAGGA ATGAGAGATT GAGAAGGGAA AGTGACGTC  
GACGTCTCTC TCTTCTCCT TACTCTCTAA CTCTTCCCTT TCACATGCAG

## Left Arm Donor Plasmid

~~~~~  
Human B7.1 Coding Region

~~~~~  
1651 CTGTATAATT TTTATCTCGA GCCCGGGAAG CTTGAATTCT TTTTATTGAT  
GACATATTAA AAATAGAGCT CGGGCCCTTC GAACTTAAGA AAAATAACTA

## ALVAC Left Arm Flanking Sequence

~~~~~  
Left Arm Donor Plasmid

~~~~~  
1701 TAACTAGTCA AATGAGTATA TATAATTGAA AAAGTAAAAT ATAAATCATA  
ATTGATCAGT TTACTCATAT ATATTAACCT TTTCATTTTA TATTTAGTAT

## ALVAC Left Arm Flanking Sequence

~~~~~  
1751 TAATAATGAA ACGAAATATC AGTAATAGAC AGGAACTGGC AGATTCTTCT
ATTATTACTT TGCTTTATAG TCATTATCTG TCCTTGACCG TCTAAGAAGA

ALVAC Left Arm Flanking Sequence

~~~~~  
1801 TCTAATGAAG TAAGTACTGC TAAATCTCCA AAATTAGATA AAAATGATAC  
AGATTACTTC ATTCATGACG ATTTAGAGGT TTTAATCTAT TTTTACTATG

## ALVAC Left Arm Flanking Sequence

~~~~~  
1851 AGCAAATACA GCTTCATTCA ACGAATTACC TTTTAATTTT TTCAGACACA
TCGTTTATGT CGAAGTAAGT TGCTTAATGG AAAATTAAAA AAGTCTGTGT

ALVAC Left Arm Flanking Sequence

~~~~~  
1901 CCTTATTACA AACTAACTAA GTCAGATGAT GAGAAAGTAA ATATAAATTT  
GGAATAATGT TTGATTGATT CAGTCTACTA CTCTTTCATT TATATTTAA

## ALVAC Left Arm Flanking Sequence

~~~~~  
1951 AACTTATGGG TATAATATAA TAAAGATTCA TGATATTAAT AATTTACTTA
TTGAATACCC ATATTATATT ATTTCTAAGT ACTATAATTA TTAAATGAAT

ALVAC Left Arm Flanking Sequence

~~~~~  
2001 ACGATGTTAA TAGACTTATT CCATCAACCC CTTCAAACCT TTCTGGATAT  
TGCTACAATT ATCTGAATAA GGTAGTTGGG GAAGTTTGGG AAGACCTATA

## ALVAC Left Arm Flanking Sequence

~~~~~  
2051 TATAAAATAC CAGTTAATGA TATTAAAATA GATTGTTTAA GAGATGTAAA
ATATTTTATG GTCAATTACT ATAATTTTAT CTAACAAATT CTCTACATTT

ALVAC Left Arm Flanking Sequence

~~~~~  
2101 TAATTATTTG GAGGTAAAGG ATATAAAATT AGTCTATCTT TCACATGGAA  
ATTAATAAAC CTCCATTTCC TATATTTTAA TCAGATAGAA AGTGTACCTT

## ALVAC Left Arm Flanking Sequence

~~~~~  
2151 ATGAATTACC TAATATTAAT AATTATGATA GGAATTTTTT AGGATTTACA
TACTTAATGG ATTATAATTA TTAATACTAT CCTTAAAAA TCCTAAATGT

ALVAC Left Arm Flanking Sequence

~~~~~  
2201 GCTGTTATAT GTATCAACAA TACAGGCAGA TCTATGGTTA TGGTAAAACA  
CGACAATATA CATAGTTGTT ATGTCCGTCT AGATACCAAT ACCATTTTGT

## ALVAC Left Arm Flanking Sequence

~~~~~  
2251 CTGTAACGGG AAGCAGCAT
GACATTGCCC TTCGTCGTA

FIGURE 13

C3R Arm
~~~~~  
1 ATATTATTAA AACTATTAGA TAACATAGCT TTATGTAAAG GAGTATTTC  
TATAATAATT TTGATAATCT ATTGTATCGA AATACATTTC CTCATAAAGG

C3R Arm  
~~~~~  
51 AGATAACTTA GCTTTAGCAT TTACGTAAGC ACCGTGGTCA AGTAAGAGTT
TCTATTGAAT CGAAATCGTA AATGCATTTC TGGCACCAGT TCATTCTCAA

C3R Arm
~~~~~  
101 TAACAAATTC TGTTTTTATA GAACTAACTG CCATGTATAG AGGAGTGAAA  
ATTGTTTAAG ACAAAGTAT CTTGATTGAC GGTACATATC TCCTCACTTT

C3R Arm  
~~~~~  
151 CCTTTATGAT TATAGACGTT TACATAGCAA CCATATAATA AGATCGCATT
GGAAATACTA ATATCTGCAA ATGTATCGTT GGTATATTAT TCTAGCGTAA

C3R Arm
~~~~~  
201 CAGTATATTA ATATCTTTCA TTTCTATAGC TATGTGAATA ACATGTTTAT  
GTCATATAAT TATAGAAAGT AAAGATATCG ATACACTTAT TGTACAAATA

C3R Arm  
~~~~~  
251 CTAATCCTAC CAACTTTGTA TCAGTACCGT ACTTCAGTAA TAAGTTTACT
GATTAGGATG GTTGAAACAT AGTCATGGCA TGAAGTCATT ATTCAAATGA

C3R Arm
~~~~~  
301 ATAGTTTGT TTTTAGATGC AACAGCTATA TTTAGAACGG TATCTATATG  
TATCAAAACA AAAATCTACG TTGTCGATAT AAATCTTGCC ATAGATATAC

## C3R Arm

~~~~~  
351 ATTATTAACC ACATTAACAT TAGATCCTCT TTCTAAAAGT GTCTTTGTTG
TAATAATTGG TGTAATTGTA ATCTAGGAGA AAGATTTTCA CAGAAACAAC

C3R Arm

~~~~~  
401 TTTCGATATC GTTACGTGAA ACAGCGTAAT GTAAGGGACT GCCCATAACG  
AAAGCTATAG CAATGCACTT TGTCGCATTA CATTCCCTGA CGGGTATGTC

## C3R Arm

~~~~~  
451 TCATCTATTA CGTTTATATC AGCTCCTAGA TTTAACAGAA GTGCTGTTAC
AGTAGATAAT GCAAATATAG TCGAGGATCT AAATTGTCTT CACGACAATG

C3R Arm

~~~~~  
501 ATCTTTTCTT CTATTAATTA CCGAATGATG TAATGGGGTT TTACCTAAAT  
TAGAAAAGAA GATAATTAAT GGCTTACTAC ATTACCCCAA AATGGATTTA

## C3R Arm

~~~~~  
551 CATCTTGTTT GTTTATAGGC ACTCCGTGAT TTATAAGTAA CGCTATTATA
GTAGAACAAG CAAATATCCG TGAGGCACTA AATATTCATT GCGATAATAT

C3R Arm

~~~~~  
601 TCGTAACTAC AATTATTTTT AAGTGCCTTT ATGAGATACT GTTTATGCAA  
AGCATTGATG TTAATAAAAA TTCACGGAAA TACTCTATGA CAAATACGTT

## C3R Arm

~~~~~  
651 AAATAAACTT TTATCTATTT TAATACTATT ATCTAACAAT ATCCTAATTA
TTTATTTGAA AATAGATAAA ATTATGATAA TAGATTGTTA TAGGATTAAT

C3R Arm

~~~~~  
701 AATCTATATT CTTATACTTT ATAGCGTAAT GTAACGGAGT TTCAAAATTT  
TTAGATATAA GAATATGAAA TATCGCATTA CATTGCCTCA AAGTTTAA

## C3R Arm

~~~~~  
751 CTAGTTTGTA TATTAAGATC AATATTAAAA TCTATAAATA TTTTATACAT
GATCAAACAT ATAATTCTAG TTATAATTTT AGATATTTAT AAAATATGTA

C3R Arm

~~~~~  
801 ATCATCAGAT ATCTTATCAT ACAGTACATC GTAATAATTT AGAAAGAATC  
TAGTAGTCTA TAGAATAGTA TGTCATGTAG CATTATTAAA TCTTCTTAG

## C3R Arm

~~~~~  
851 TATTACAATT AACACCTTTT TTAATAAAT ATCTAGTTAA TGACTTATTG
ATAATGTAA TTGTGAAAA AAATTATTTA TAGATCAATT ACTGAATAAC

C3R Arm

901 TTTCTATATA CAGAAATATA TAACGGACTA TTTCCAGAAT GTATCTGTTT
AAAGATATAT GTCTTTATAT ATTGCCTGAT AAAGGTCTTA CATAGACAAG

C3R Arm

951 TATGTCAGCG CCAGAATCTA TTAGTAGTTT AGCAATTCT GTATTATCTA
ATACAGTCGC GGTCTTAGAT AATCATCAAA TCGTTAAAGA CATAATAGAT

C3R Arm

1001 AACTAGCAGC TTTATGAAGA GGAGGATTTT TACATTTTAA AATATCGGCA
TTGATCGTCG AAATACTTCT CCTCCTAAAA ATGTAAAATT TTATAGCCGT

C3R Arm

1051 CCGTGTCTA GTAATAATTT TACCATTCT ATATCAGAAA TACTTACGGC
GGCACAAGAT CATTATTAAA ATGGTAAAGA TATAGTCTTT ATGAATGCCG

C3R Arm

1101 TAAATACAAA GACGTTGATA GTATATTTAC GTTATTGTAT TTGCATTTTT
ATTTATGTTT CTGCAACTAT CATATAAATG CAATAACATA AACGTAAAAA

C3R Arm

1151 TAAGTATATA CCTTACTAAA TTTATATCTC TATACCTTAT AGCTTTATGC
ATTCATATAT GGAATGATTT AAATATAGAG ATATGGAATA TCGAAATACG

C3R Arm

1201 AGTTCATTTA TAAGTCTTCC ATTACTCATT TCTGGTAATG AAGTATTATA
TCAAGTAAAT ATTCAGAAGG TAATGAGTAA AGACCATTAC TTCATAATAT

C3R Arm

1251 TATCATTATG ATATTATCTC TATTTTATTC TAATAAAAAC CGTTATCATG
ATAGTAATAC TATAATAGAG ATAAATAAG ATTATTTTGG GCAATAGTAC

C3R Arm

1301 TTATTTATTA TTTGTTATAA TTATACTATT TAATAAATTA TACCAAATAC
AATAAATAAT AAACAATATT AATATGATAA ATTATTTAAT ATGGTTTATG

C3R Arm

1351 TTAGATACTT ATTAATACCA TCCTAGAACT TGTATTTCTT GCCCCCTAAA
AATCTATGAA TAATTATGGT AGGATCTTGA ACATAAAGAA CGGGGGATTT

C3R Arm

1401 CTTGGACATG CACTCCATTA GCGTTTTCTT GTTTTCGACA TCGTCCTCCT
GAACCTGTAC GTGAGGTAAT CCGCAAAGAA CAAAAGCTGT AGCAGGAGGA

C3R Arm

1451 ~~~~~
TAACATATCC TACTGTTATG TGAGGATTCC ACGGATTATC TACTGTGATA
ATTGTATAGG ATGACAATAC ACTCCTAAGG TGCCTAATAG ATGACACTAT

C3R Arm

1501 ~~~~~
TCACCAAACA CGTCCTTCGA ACAGGGTACC GCATTGAGCA GAACATTTCT
AGTGGTTTGT GCAGGAAGCT TGTCCCATGG CGTAAGTCGT CTTGTAAAGA

C3R Arm

1551 ~~~~~
TAGGGCTCTA AGTTCATCAG ATACCTCCAG TTTCATAACT ACAGCGCATC
ATCCCGAGAT TCAAGTAGTC TATGGAGGTC AAAGTATTGA TGTGCGTAG

C3R Arm

1601 ~~~~~
CTTTCGCTCC CAACTGTTTA GAGGCGTTAC TCTGAGGAAA ACACATCTCT
GAAAGCGAGG GTTGACAAAT CTCCGCAATG AGACTCCTTT TGTGTAGAGA

C3R Arm

1651 ~~~~~
TCTTTACAGA CTATAGAAAT AGTCTGTAAA TCTTGATCAG TTATTTGCTT
AGAAATGTCT GATATCTTTA TCAGACATTT AGAACTAGTC AATAAACGAA

C3R Arm

1701 ~~~~~
TTTGAAATTT TCAAATCTAT CACATTGATC CATATTTGCT ATTCCAAGAG
AAACTTTAAA AGTTTAGATA GTGTAAC TAGTATAAACGA TAAGGTTCTC

C3R Arm

1751 ~~~~~
TTATATGAGG AAAAATATCA CATCCTGTCA TGTATTTTAT TGTAACATTA
AATATACTCC TTTTATAGT GTAGGACAGT ACATAAAATA ACATTGTAAT

C3R Arm

1801 ~~~~~
TTATAATCTG TAACATCAGT ATCTAACCTA ACGTCGTAAA AGTTAACAGA
AATATTAGAC ATTGTAGTCA TAGATTGGAT TGCAGCATTT TCAATTGTCT

C3R Arm

1851 ~~~~~
TGCCAGTTA CTATAATCCC AAGGAACCTT AACATCTAAT CCCATTAAAA
ACGGGTCAAT GATATTAGG TTCCTTGGA TGTAGATTA GGGTAATTTT

C3R Arm

1901 ~~~~~
TAGTATCCTT TCTACTATTT TTTTCATTGG CAAGTATGTG GCTTAGTTTA
ATCATAGGAA AGATGATAAA AAAAGTAACC GTTCATACAC CGAATCAAAT

C3R Arm

1951 ~~~~~
CACAAAATTC CTGCCATTTT GTAACGATAG CGAAGCAATA GCTTGTATGC
GTGTTTAAAG GACGGTAAAA CATTGCTATC GCTTCGTTAT CGAACATACG

H6 promoter
~~~~~  
2001 TTTTATTG ATTAAGTAGT CATAAAATC GGGATCCTTC TTTATTCTAT  
AAAAATAAAC TAATTGATCA GTATTTTAG CCCTAGGAAG AAATAAGATA

H6 promoter  
~~~~~  
2051 ACTTAAAAAG TGAAAATAAA TACAAAGGTT CTTGAGGGTT GTGTTAAATT
TGAATTTTTC ACTTTTATTT ATGTTTCCAA GAACTCCCAA CACAATTTAA

H6 promoter
~~~~~  
2101 GAAAGCGAGA AATAATCATA AATTATTTCA TTATCGCGAT ATCCGTTAAG  
CTTTCGCTCT TTATTAGTAT TTAATAAAGT AATAGCGCTA TAGGCAATTC

MCEA  
~~~~~  
H6 promoter
~~~~~  
2151 TTTGTATCGT AATGGAGTCT CCCTCGGCCC GTCCCCACAG ATGGTGCATC  
AAACATAGCA TTACCTCAGA GGGAGCCGGG GAGGGGTGTC TACCACGTAG

MCEA  
~~~~~  
2201 CCCTGGCAGA GGCTCCTGCT CACAGCCTCA CTCTAACCT TCTGGAACCC
GGGACCGTCT CCGAGGACGA GTGTCGGAGT GAAGATTGGA AGACCTTGGG

MCEA
~~~~~  
2251 GCCCACCCT GCCAAGCTCA CTATTGAATC CACGCCGTTT AATGTCGCAG  
CGGGTGGTGA CGGTTTCGAGT GATAACTTAG GTGCGGCAAG TTACAGCGTC

MCEA  
~~~~~  
2301 AGGGGAAGGA GGTGCTTCTA CTTGTCCACA ATCTGCCCA GCATCTTTT
TCCCCCTCCT CCACGAAGAT GAACAGGTGT TAGACGGGGT CGTAGAAAAA

MCEA
~~~~~  
2351 GGCTACAGCT GGTACAAAGG TGAAAGAGTG GATGGCAACC GTCAAATTAT  
CCGATGTCGA CCATGTTTCC ACTTTCTCAC CTACCGTTGG CAGTTTAATA

MCEA  
~~~~~  
2401 AGGATATGTA ATAGGAAGTC AACAAGCTAC CCCAGGGCCC GCATACAGTG
TCCTATACAT TATCCTTGAG TTGTTTCGATG GGGTCCCGGG CGTATGTCAC

MCEA
~~~~~  
2451 GTCGAGAGAT AATATACCCC AATGCATCCC TGCTGATCCA GAACATCATC  
CAGCTCTCTA TTATATGGGG TTACGTAGGG ACGACTAGGT CTTGTAGTAG

MCEA  
~~~~~  
2501 CAGAATGACA CAGGATTCTA CACCCTACAC GTCATAAAGT CAGATCTTGT
GTCTTACTGT GTCCTAAGAT GTGGGATGTG CAGTATTTCA GTCTAGAACA

MCEA

2551 ~~~~~
GAATGAAGAA GCAACTGGCC AGTTCCGGGT ATACCCGGAA CTCCCTAAGC
CTTACTTCTT CGTTGACCGG TCAAGGCCCA TATGGGCCTT GAGGGATTCTG

MCEA

2601 ~~~~~
CTTCTATTAG CTCCAATAAT AGTAAGCCTG TCGAAGACAA AGATGCCGTC
GAAGATAATC GAGGTTATTA TCATTCCGAC AGCTTCTGTT TCTACGGCAG

MCEA

2651 ~~~~~
GCTTTTACAT GCGAGCCCGA AACTCAAGAC GCAACATATC TCTGGTGGGT
CGAAAATGTA CGCTCGGGCT TTGAGTTCTG CGTTGTATAG AGACCACCCA

MCEA

2701 ~~~~~
GAACAACCAG TCCCTGCCTG TGTCCCCTAG ACTCCAATC AGCAACGGAA
CTTGTTGGTC AGGGACGGAC ACAGGGGATC TGAGGTTGAG TCGTTGCCTT

MCEA

2751 ~~~~~
ATAGAACTCT GACCCTGTTT AACGTGACCA GGAACGACAC AGCAAGCTAC
TATCTTGAGA CTGGGACAAA TTGCACTGGT CCTTGCTGTG TCGTTCGATG

MCEA

2801 ~~~~~
AAATGCGAAA CCCAAAATCC AGTCAGCGCC AGGAGGTCTG ATTCACTGAT
TTTACGCTTT GGGTTTTAGG TCAGTCGCGG TCCTCCAGAC TAAGTCACTA

MCEA

2851 ~~~~~
TCTCAACGTG CTTTACGGAC CCGATGCTCC TACAATCAGC CCTCTAAACA
AGAGTTGCAC GAAATGCCTG GGCTACGAGG ATGTTAGTCG GGAGATTTGT

MCEA

2901 ~~~~~
CAAGCTATAG ATCAGGGGAA AATCTGAATC TGAGCTGTCA TGCCGCTAGC
GTTGATATC TAGTCCCCTT TTAGACTTAG ACTCGACAGT ACGGCGATCG

MCEA

2951 ~~~~~
AATCCTCCCG CCCAATACAG CTGGTTTGTC AATGGCACTT TCCAACAGTC
TTAGGAGGGC GGGTTATGTC GACCAAACAG TTACCGTGAA AGGTTGTCAG

MCEA

3001 ~~~~~
CACCAGGAA CTGTTCAATC CCAATATTAC CGTGAACAAT AGTGGATCCT
GTGGGTCCTT GACAAGTAAG GGTATAATG GCACTTGTTA TCACCTAGGA

MCEA

3051 ~~~~~
ACACGTGCCA AGCTCACAAT AGCGACACCG GACTCAACCG CACAACCGTG
TGTGCACGGT TCGAGTGTTA TCGCTGTGGC CTGAGTTGGC GTGTTGGCAC

MCEA

3101 ~~~~~
ACGACGATTA CCGTGTATGA GCCACCAAAA CCATTCATAA CTAGTAACAA
TGCTGCTAAT GGCACATACT CCGTGGTTTT GGTAAGTATT GATCATTGTT

MCEA

3151 ~~~~~
TTCTAACCCA GTTGAGGATG AGGACGCAGT TGCATTAACT TGTGAGCCAG
AAGATTGGGT CAACTCCTAC TCCTGCGTCA ACCTAATTGA ACACTCGGTC

MCEA

3201 ~~~~~
AGATTCAAAA TACCACTTAT TTATGGTGGG TCAATAACCA AAGTTTGCCG
TCTAAGTTTT ATGGTGAATA AATACCACCC AGTTATTGGT TTCAAACGGC

MCEA

3251 ~~~~~
GTTAGCCAC GCTTGCAGTT GTCTAATGAT AACCGCACAT TGACACTCCT
CAATCGGGTG CGAACGTCAA CAGATTACTA TTGGCGTGTA ACTGTGAGGA

MCEA

3301 ~~~~~
GTCCGTTACT CGCAATGATG TAGGACCTTA TGAGTGTGGC ATTCAGAATG
CAGGCAATGA GCGTTACTAC ATCCTGGAAT ACTCACACCG TAAGTCTTAC

MCEA

3351 ~~~~~
AATTATCCGT TGATCACTCC GACCCTGTTA TCCTTAATGT TTTGTATGGC
TTAATAGGCA ACTAGTGAGG CTGGGACAA AGGAATTACA AAACATACCG

MCEA

3401 ~~~~~
CCAGACGACC CAACTATATC TCCATCATAAC ACCTACTACC GTCCCGGCGT
GGTCTGCTGG GTTGATATAG AGGTAGTATG TGGATGATGG CAGGGCCGCA

MCEA

3451 ~~~~~
GAACTTGAGC CTTTCTTGCC ATGCAGCATC CAACCCCCCT GCACAGTACT
CTTGAACCTG GAAAGAACGG TACGTCGTAG GTGGGGGGA CGTGTCATGA

MCEA

3501 ~~~~~
CCTGGCTGAT TGATGGAAAC ATTCAGCAGC ATACTCAAGA GTTATTTATA
GGACCGACTA ACTACCTTTG TAAGTCGTCG TATGAGTTCT CAATAAATAT

MCEA

3551 ~~~~~
AGCAACATAA CTGAGAAGAA CAGCGGACTC TATACTTGCC AGGCCAATAA
TCGTTGTATT GACTCTTCTT GTCGCCTGAG ATATGAACGG TCCGGTTATT

MCEA

3601 ~~~~~
CTCAGCCAGT GGTCACAGCA GGACTACAGT TAAACAATA ACTGTTTCCG
GAGTCGGTCA CCAGTGTCGT CCTGATGTCA ATTTTGTTAT TGACAAAGGC

MCEA

3651 ~~~~~
CGGAGCTGCC CAAGCCCTCC ATCTCCAGCA ACAACTCCAA ACCCGTGGAG
GCCTCGACGG GTTCGGGAGG TAGAGGTCGT TGTGAGGTT TGGGCACCTC

MCEA

3701 ~~~~~
GACAAGGATG CTGTGGCCTT CACCTGTGAA CCTGAGGCTC AGAACACAAC
CTGTTCTTAC GACACCGGAA GTGGACACTT GGACTCCGAG TCTTGTGTTG

MCEA

3751 ~~~~~
CTACCTGTGG TGGGTAAATG GTCAGAGCCT CCCAGTCAGT CCCAGGCTGC
GATGGACACC ACCCATTAC CAGTCTCGGA GGGTCAGTCA GGGTCCGACG

MCEA

3801 ~~~~~
AGCTGTCCAA TGGCAACAGG ACCCTCACTC TATTCAATGT CACAAGAAAT
TCGACAGGTT ACCGTTGTCC TGGGAGTGAG ATAAGTTACA GTGTTCTTTA

MCEA

3851 ~~~~~
GACGCAAGAG CCTATGTATG TGGAATCCAG AACTCAGTGA GTGCAAACCG
CTGCGTTCTC GGATACATAC ACCTTAGGTC TTGAGTCACT CACGTTTGGC

MCEA

3901 ~~~~~
CAGTGACCCA GTCACCCTGG ATGTCCTCTA TGGGCCGGAC ACCCCATCA
GTCAGTGGT CAGTGGGACC TACAGGAGAT ACCCGCCTG TGGGGGTAGT

MCEA

3951 ~~~~~
TTTCCCCCCC AGACTCGTCT TACCTTTCGG GAGCGAACCT CAACCTCTCC
AAAGGGGGGG TCTGAGCAGA ATGGAAAGCC CTCGCTTGA GTTGGAGAGG

MCEA

4001 ~~~~~
TGCCACTCGG CCTCTAACCC ATCCCCGCAG TATTCTTGGC GTATCAATGG
ACGGTGAGCC GGAGATTGGG TAGGGGCGTC ATAAGAACCG CATAGTTACC

MCEA

4051 ~~~~~
GATACCGCAG CAACACACAC AAGTTCTCTT TATCGCCAA ATCAGCCAA
CTATGGCGTC GTTGTGTGTG TTCAAGAGAA ATAGCGGTTT TAGTGCGGTT

MCEA

4101 ~~~~~
ATAATAACGG GACCTATGCC TGTTTGTCT CTAAGTTGGC TACTGGCCGC
TATTATTGCC CTGGATACGG ACAAACAGA GATTGAACCG ATGACCGGCG

MCEA

4151 ~~~~~
AATAATTCCA TAGTCAAGAG CATCACAGTC TCTGCATCTG GAACTTCTCC
TTATTAAGGT ATCAGTTCTC GTAGTGTGAG AGACGTAGAC CTTGAAGAGG

MCEA

~~~~~  
4201 TGGTCTCTCA GCTGGGGCCA CTGTCGGCAT CATGATTGGA GTGCTGGTTG  
ACCAGAGAGT CGACCCCGGT GACAGCCGTA GTACTAACCT CACGACCAAC

## MCEA

~~~~~  
4251 GGGTTGCTCT GATATAGTTT TTATCTCGAG GAATTCCTGC AGCCCGGGTT
CCCAACGAGA CTATATCAAA AATAGAGCTC CTTAAGGACG TCGGGCCCAA

C3L Arm

~~~~~  
4301 TTTATAGCTA ATTAGTCAAA TGTGAGTTAA TATTAGTATA CTACATTACT  
AAATATCGAT TAATCAGTTT AACTCAATT ATAATCATAT GATGTAATGA

## C3L Arm

~~~~~  
4351 AATTTATTAC ATATTCATTT ATATCAATCT AGTAGCATT AGCTTTTATA
TTAAATAATG TATAAGTAA TATAGTTAGA TCATCGTAA TCGAAATAT

C3L Arm

~~~~~  
4401 AAACAATATA ACTGAATAGT ACATACTTTA CTAATAAGTT ATAAATAAGA  
TTTGTATAT TGACTTATCA TGTATGAAAT GATTATTCOA TATTTATTCT

## C3L Arm

~~~~~  
4451 GATACATATT TATAGTATTT TACTTTCTAC ACTGAATATA ATAATATAAT
CTATGTATAA ATATCATAAA ATGAAAGATG TGACTTATAT TATTATATTA

C3L Arm

~~~~~  
4501 TATACAAATA TAATTTTTTAA TACTATATAG TATATAACTG AAATAAAATA  
ATATGTTTAT ATTAAAAATT ATGATATATC ATATATTGAC TTTATTTTAT

## C3L Arm

~~~~~  
4551 CCAGTGTAAT ATAGTTATTA TACATTTATA CCACATCAAA GATGAGTTAT
GGTCACATTA TATCAATAAT ATGTAAATAT GGTGTAGTTT CTAATCAATA

C3L Arm

~~~~~  
4601 AACATCAGTG TCACTGTTAG CAACAGTAGT TATACGATGA GTAGTTACTC  
TTGTAGTCAC AGTGACAATC GTTGTCATCA ATATGCTACT CATCAATGAG

## C3L Arm

~~~~~  
4651 TCGTATGGCG TTAGTATGTA TGTATCTTCT AGTTTCTTA GTAGGCATTA
AGCATACCGC AATCATACAT ACATAGAAGA TCAAAAGAAT CATCCGTAAT

C3L Arm

~~~~~  
4701 TAGGAAACGT CAAGCTTATA AGGTTATTAA TGGTATCTAG AAATATATCT  
ATCCTTTGCA GTTCGAATAT TCCAATAATT ACCATAGATC TTTATATAGA

## C3L Arm

~~~~~  
4751 ATTATACCGT TTCTCAACTT GGAATAGCC GATTGCTGT TTGTGATATT
TAATATGGCA AAGAGTTGAA CCCTTATCGG CTAAACGACA AACACTATAA

C3L Arm

~~~~~  
4801 CATACCTTTA TACATTATAT ACATACTAAG TAATTTCAT TGGCATTTTG  
GTATGGAAAT ATGTAATATA TGTATGATTC ATTAAAGGTA ACCGTAAAC

## C3L Arm

~~~~~  
4851 GTAAAGCACT TTGTAAAATT AGTTCTTTCT TTTTACTTC TAACATGTTT
CATTTCTGTA AACATTTTAA TCAAGAAAGA AAAAATGAAG ATTGTACAAA

C3L Arm

~~~~~  
4901 GCAAGTATAT TTTAATAAC TGTAATAAGC GTATATAGAT ATGTAAAAAT  
CGTTCATATA AAAATTATTG ACATTATTCG CATATATCTA TACATTTTAA

## C3L Arm

~~~~~  
4951 TACCCTTCCT GGATTTACCT ATAAATATGT TAACATTAGA AATATGTACA
ATGGGAAGGA CCTAAATGGA TATTATACA ATTGTAATCT TTATACATGT

C3L Arm

~~~~~  
5001 TTACTATATT TTTCATATGG ATTATTTCTA TTATACTAGG GATTCCTGCT  
AATGATATAA AAAGTATACC TAATAAGAT AATATGATCC CTAAGGACGA

## C3L Arm

~~~~~  
5051 CTTTACTTTA GAAATACTAT CGTAACAAA AATAACGACA CGCTGTGTAT
GAAATGAAAT CTTTATGATA GCATTGTTT TTATTGCTGT GCGACACATA

C3L Arm

~~~~~  
5101 TAATCATTAT CATGATAATA GAGAAATTGC TGAATTGATT TACAAAGTTA  
ATTAGTAATA GTACTATTAT CTCTTTAACG ACTTAACTAA ATGTTTCAAT

## C3L Arm

~~~~~  
5151 TTATCTGTAT CAGATTTATT TTAGGATACC TACTACCTAC GATAATTATA
AATAGACATA GTCTAAATAA AATCCTATGG ATGATGGATG CTATTAATAT

C3L Arm

~~~~~  
5201 CTCGTATGCT ATACGTTACT GATCTACAGA ACTAACAATG CATGTCGACG  
GAGCATACGA TATGCAATGA CTAGATGTCT TGATTGTTAC GTACAGCTGC

## C3L Arm

~~~~~  
5251 CGGCCGCAA
GCCGGCGTT

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☒ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.